

results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1108406271-19060-109558541338.BLASTQ4

Query=

(226 letters)

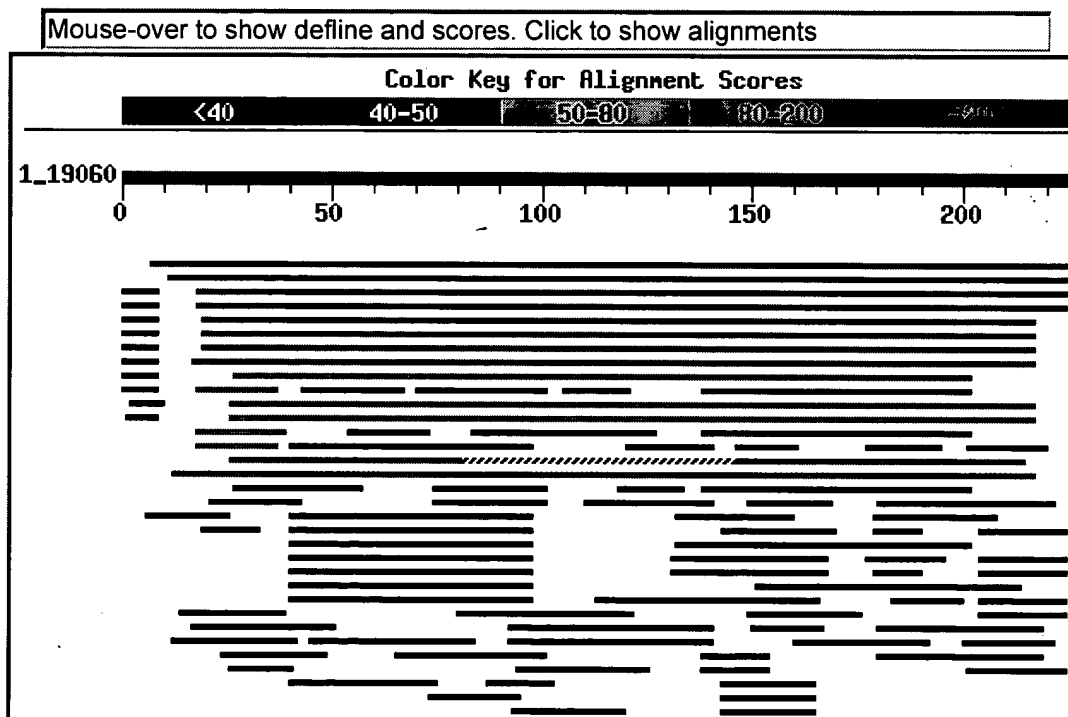
Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,326,143 sequences; 788,882,796 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 101 Blast Hits on the Query Sequence



[Related Structures](#)

| Sequences producing significant alignments: | | Score (bits) | E Value | |
|--|--|-----------------|------------|----------|
| gi 505281 emb CAA41768.1 | exoenzyme C3 [Clostridium botulin... | 630 | e-179 | |
| gi 747707 emb CAA35828.1 | exoenzyme C3 [Clostridium botulin... | 627 | e-178 | |
| gi 51247865 pdb 1UZI B | Chain B, C3 Exoenzyme From Clostridi... | 609 | e-173 | S |
| gi 23200102 pdb 1GZE D | Chain D, Structure Of The Clostridiu... | 599 | e-170 | S |
| gi 399048 sp Q00901 ARC3_CBCP | Mono-ADP-ribosyltransferase C... | 338 | 2e-91 | |
| gi 56965901 pdb 1R4B B | Chain B, Adp-Ribosyltransferase C3bo... | 338 | 2e-91 | S |
| gi 404821 dbj BAA04492.1 | ADP-ribosyltransferase C3 [Clostr... | 328 | 1e-88 | |
| gi 1212875 emb CAA60674.1 | exoenzyme C3 [Clostridium limosu... | 316 | 7e-85 | |
| gi 22795813 emb CAD22164.1 | ADP-ribosyltransferase [Bacillu... | 77 | 1e-12 | |
| gi 236587 gb AAB19984.1 | ADP-ribosyltransferase exoenzyme C... | 70 | 1e-10 | |
| gi 13186140 emb CAC33493.1 | ADP-ribosyltransferase [Staphyl... | 67 | 1e-09 | S |
| gi 24636605 dbj BAC22946.1 | epidermal cell differentiation ... | 67 | 1e-09 | |
| gi 80491 pir S05236 | exoenzyme C3 - Clostridium botulinum (...) | 62 | 4e-08 | |
| gi 236588 gb AAB19985.1 | ADP-ribosyltransferase exoenzyme C... | 60 | 2e-07 | |
| gi 17227179 ref NP_478345.1 | hypothetical protein [Staphylo... | 59 | 2e-07 | |
| gi 79857 pir JG0016 | epidermal cell differentiation inhibit... | 53 | 1e-05 | |
| gi 249591 gb AAB22208.1 | ADP-ribosyltransferase [Clostridiu... | 41 | 0.089 | |
| gi 249592 gb AAB22209.1 | ADP-ribosyltransferase [Clostridiu... | 40 | 0.12 | |
| gi 6730536 pdb 1QS1 D | Chain D, Crystal Structure Of Vegetat... | 40 | 0.12 | S |
| gi 6730537 pdb 1QS2 A | Chain A, Crystal Structure Of Vip2 Wi... | 40 | 0.12 | S |
| gi 29650779 gb AAO86513.1 | Vip2Ac [Bacillus thuringiensis] | 40 | 0.16 | |
| gi 435823 gb AAB28629.1 | C3-like ADP-ribosyltransferase {NA... | 38 | 0.39 | |
| gi 45219853 gb AAH66784.1 | Autoantigen La [Xenopus tropical... | 38 | 0.52 | G |
| gi 29374726 ref NP_813878.1 | lipoprotein, putative [Enteroc... | 35 | 3.0 | G |
| gi 15893630 ref NP_346979.1 | Mono-ADP-ribosyltransferase C3... | 35 | 3.0 | G |
| gi 21315078 gb AAH30775.1 | ARTS-1 protein [Homo sapiens] >g... | 35 | 4.0 | G |
| gi 37182302 gb AAQ88953.1 | ARTS-1 [Homo sapiens] | 35 | 4.0 | G |
| gi 6642987 gb AAF20384.1 | aminopeptidase PILS [Homo sapiens] | 35 | 4.0 | G |
| gi 6381989 gb AAF07395.1 | adipocyte-derived leucine aminope... | 35 | 4.0 | G |
| gi 19879276 gb AAK37778.1 | adipocyte-derived leucine aminop... | 35 | 4.0 | G |
| gi 23509168 ref NP_701836.1 | hypothetical protein PFL2380c ... | 35 | 4.0 | G |
| gi 55625752 ref XP_527213.1 | PREDICTED: similar to adipocyt... | 35 | 4.0 | G |
| gi 20137531 sp Q9NZ08 ART1_HUMAN | Adipocyte-derived leucine ... | 35 | 4.0 | G |
| gi 20521069 dbj BAA25451.2 | KIAA0525 protein [Homo sapiens] | 35 | 4.0 | G |
| gi 29655312 ref NP_821004.1 | adenosylhomocysteinase [Coxiel... | 35 | 5.4 | G |
| gi 64876 emb CAA48716.1 | La protein form B [Xenopus laevis]... | 34 | 7.3 | G |
| gi 28436825 gb AAH46654.1 | MGC52876 protein [Xenopus laevis] | 34 | 7.3 | G |
| gi 50083934 ref YP_045444.1 | hypothetical protein; putative... | 34 | 7.3 | G |
| gi 2344808 emb CAB05387.1 | unknown [Helicobacter pylori] | 34 | 7.3 | |
| gi 18144707 dbj BAB80752.1 | hypothetical protein [Clostridi... | 34 | 7.3 | G |
| gi 1006663 emb CAA84542.1 | MDR3 P-glycoprotein [Homo sapiens] | 34 | 9.8 | G |
| gi 51473693 ref YP_067450.1 | rickettsial conserved hypothet... | 34 | 9.8 | G |
| gi 48847109 ref ZP_00301367.1 | COG0443: Molecular chaperone... | 34 | 9.8 | |
| gi 48844634 ref ZP_00298937.1 | hypothetical protein Gmet020... | 34 | 9.8 | |
| gi 48844300 ref ZP_00298619.1 | COG0525: Valyl-tRNA syntheta... | 34 | 9.8 | |
| gi 48844054 ref ZP_00298396.1 | COG2025: Electron transfer f... | 34 | 9.8 | |
| gi 48843994 ref ZP_00298350.1 | hypothetical protein Gmet020... | 34 | 9.8 | |
| gi 34764189 ref ZP_00145051.1 | TYPE I RESTRICTION-MODIFICAT... | 34 | 9.8 | |

| | | | | |
|--|---|--------------------|-----|----------|
| gi 2313683 gb AAD07632.1 | H. pylori predicted coding region... | 34 | 9.8 | G |
| gi 41723241 ref ZP_00150184.1 | COG0642: Signal transduction... | 34 | 9.8 | |
| gi 39594284 emb CAE71862.1 | Hypothetical protein CBG18908 [...] | 34 | 9.8 | |
| gi 39583135 emb CAE60675.1 | Hypothetical protein CBG04328 [...] | 34 | 9.8 | |
| gi 14276022 dbj BAB58942.1 | phenol hydroxylase large subuni... | 34 | 9.8 | |
| gi 730030 sp P40631 MLH_TETH | Micronuclear linker histone p... | 33 | 13 | |
| gi 57208133 emb CAI40768.1 | Isp2a protein [Brevibacillus la... | 33 | 13 | |
| gi 51556700 ref YP_068061.1 | pTP [Tree shrew adenovirus] | 33 | 13 | G |
| gi 27468972 ref NP_765609.1 | hypothetical protein SE2054 [S... | 33 | 18 | G |
| gi 57865475 ref YP_189623.1 | membrane protein, putative [St... | 33 | 18 | G |
| gi 53687109 ref ZP_00107385.2 | COG1177: ABC-type spermidine... | 33 | 18 | |
| gi 51013377 gb AAT92982.1 | YHR005C [Saccharomyces cerevisia... | 32 | 24 | G |
| gi 173560 gb AAA18403.1 | putative. G-alpha-like protein | 32 | 24 | |
| gi 24377635 gb AAN58940.1 | conserved hypothetical protein; ... | 32 | 24 | G |
| gi 7511574 pir T18747 | probable potassium channel protein -... | 32 | 24 | |
| gi 48733274 ref ZP_00267017.1 | COG3451: Type IV secretory p... | 32 | 32 | |
| gi 30022154 ref NP_833785.1 | Stage V sporulation protein AD... | 32 | 32 | G |
| gi 47529582 ref YP_020931.1 | stage v sporulation protein ad... | 32 | 32 | G |
| gi 50906527 ref XP_464752.1 | putative pentatricopeptide (PP... | 32 | 32 | G |
| gi 52141425 ref YP_085404.1 | stage V sporulation protein AD... | 32 | 32 | G |
| gi 42783182 ref NP_980429.1 | stage V sporulation protein AD... | 32 | 32 | G |
| gi 48870644 ref ZP_00323364.1 | COG3010: Putative N-acetylma... | 32 | 32 | |
| gi 48854717 ref ZP_00308878.1 | COG5651: PPE-repeat proteins... | 32 | 32 | |
| gi 47565952 ref ZP_00236991.1 | stage V sporulation protein ... | 32 | 32 | |
| gi 53687444 ref ZP_00108980.2 | COG4644: Transposase and ina... | 32 | 32 | |
| gi 39587376 emb CAE75030.1 | Hypothetical protein CBG22937 [...] | 32 | 32 | |
| gi 454862 gb AAA69970.1 | region near C-terminus; putative | 32 | 32 | |
| gi 16081318 ref NP_393636.1 | hypothetical protein Ta0158 [T... | 32 | 43 | G |
| gi 54641100 gb EAL29851.1 | GA20157-PA [Drosophila pseudoobs... | 32 | 43 | |
| gi 52352362 gb AAU43652.1 | FAD/FMN-containing dehydrogenase... | 32 | 43 | |
| gi 15828932 ref NP_326292.1 | hypothetical protein MYPU_4610... | 31 | 57 | G |
| gi 34104158 gb AAQ60517.1 | conserved hypothetical protein [...] | 31 | 57 | G |
| gi 27467268 ref NP_763905.1 | penicillin amidase V [Staphylo... | 31 | 57 | G |
| gi 49474859 ref YP_032900.1 | Adenosylhomocysteinase [Barton... | 31 | 57 | G |
| gi 57168708 ref ZP_00367840.1 | conserved hypothetical prote... | 31 | 57 | |
| gi 41409460 ref NP_962296.1 | SahH [Mycobacterium avium subs... | 31 | 57 | G |
| gi 29653858 ref NP_819550.1 | excinuclease ABC, B subunit [C... | 31 | 57 | G |
| gi 52549567 gb AAU83416.1 | FAD FMN containing dehydrogenase... | 31 | 57 | |
| gi 30025120 gb AAC69093.2 | Innexin protein 5 [Caenorhabditi... | 31 | 57 | |
| gi 28828803 gb AAO51398.1 | hypothetical protein [Dictyostel... | 31 | 57 | |
| gi 50308841 ref XP_454425.1 | unnamed protein product [Kluyv... | 31 | 57 | G |
| gi 48097538 ref XP_391917.1 | similar to CG11654-PA [Apis me... | 31 | 57 | G |
| gi 57866161 ref YP_187823.1 | penicillin V acylase, putative... | 31 | 57 | G |
| gi 17568579 ref NP_509403.1 | innexin, putative gap junction... | 31 | 57 | G |
| gi 53735789 ref ZP_00178447.2 | hypothetical protein Cwat030... | 31 | 57 | |
| gi 46143226 ref ZP_00135639.2 | COG1404: Subtilisin-like ser... | 31 | 57 | |
| gi 39583806 emb CAE74879.1 | Hypothetical protein CBG22739 [...] | 31 | 57 | |
| gi 38491955 gb AAR22310.1 | mitochondrial intermediate pepti... | 31 | 57 | |
| gi 51534847 dbj BAD37204.1 | nitrite reductase [uncultured b... | 31 | 57 | |
| gi 236586 gb AAB19983.1 | ADP-ribosyltransferase exoenzyme C... | 31 | 57 | |
| gi 54020612 ref YP_116107.1 | DNA polymerase III alpha chain... | 31 | 77 | G |
| gi 53729791 ref ZP_00150191.2 | COG2887: RecB family exonucl... | 31 | 77 | |

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|505281|emb|CAA41768.1| exoenzyme C3 [Clostridium botulinum D phage]
 gi|296787|emb|CAA41767.1| exoenzyme C3 [Clostridium botulinum C phage]
 gi|625586|pir||A38912 NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3 prec
 Clostridium botulinum phage (strain CST)
 gi|399049|sp|P15879|ARC3_CBDP Mono-ADP-ribosyltransferase C3 precursor (Exoenzyme
 Length = 251

Score = 630 bits (1479), Expect = e-179

Identities = 209/224 (93%), Positives = 210/224 (93%), Gaps = 7/224 (3%)

Query: 8 QACNAYSFNQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK 67
 Q C AYS NQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK
 Sbjct: 30 QKCYAYSINQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGK 89
 Query: 68 LRQNKGVINGFPSNLIQ--WLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNG 125
 LRQNKGVINGFPSNLIQ LLDKSFNKMKT PENIMLF GDDPAYLGTEFQNTLLNSNG
 Sbjct: 90 LRQNKGVINGFPSNLIQVE-LLDKSFNKMKT PENIMLFRGDDPAYLGTEFQNTLLNSNG 148
 Query: 126 TINKTAFEKAKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS 185
 TINKTAFEKAKA +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS
 Sbjct: 149 TINKTAFEKAKA-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPIS 207
 Query: 186 AFQGGLEG-LPRHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 AF GQLE LPRHSTYHIDDMRLSSDGKQIIITAT GTAINPK
 Sbjct: 208 AFAGQLEMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 251

☐ >gi|747707|emb|CAA35828.1| exoenzyme C3 [Clostridium botulinum D phage]
 Length = 218

Score = 627 bits (1472), Expect = e-178

Identities = 207/220 (94%), Positives = 208/220 (94%), Gaps = 7/220 (3%)

Query: 12 AYSFNQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN 71
 AYS NQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN
 Sbjct: 1 AYSINQKAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQN 60
 Query: 72 KGVINGFPSNLIQ--WLLDKSFNKMKT PENIMLFXGDDPAYLGTEFQNTLLNSNGTINK 129
 KGVINGFPSNLIQ LLDKSFNKMKT PENIMLF GDDPAYLGTEFQNTLLNSNGTINK
 Sbjct: 61 KGVINGFPSNLIQVE-LLDKSFNKMKT PENIMLFRGDDPAYLGTEFQNTLLNSNGTINK 119
 Query: 130 TAFEKAKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQG 189
 TAFEKAKA +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAF G
 Sbjct: 120 TAFEKAKA-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAG 178
 Query: 190 QLEG-LPRHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 QLE LPRHSTYHIDDMRLSSDGKQIIITAT GTAINPK
 Sbjct: 179 QLEMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 218

☐ >gi|51247865|pdb|1UZI|B **S** Chain B, C3 Exoenzyme From Clostridium Botulinum, Tetr
gi|51247864|pdb|1UZI|A **S** Chain A, C3 Exoenzyme From Clostridium Botulinum, Tetrag
gi|23200106|pdb|1GZF|D **S** Chain D, Structure Of The Clostridium Botulinum C3 Exoen
(Wild-Type) In Complex With Nad
gi|23200105|pdb|1GZF|C **S** Chain C, Structure Of The Clostridium Botulinum C3 Exoen
(Wild-Type) In Complex With Nad
gi|23200104|pdb|1GZF|B **S** Chain B, Structure Of The Clostridium Botulinum C3 Exoen
(Wild-Type) In Complex With Nad
gi|23200103|pdb|1GZF|A **S** Chain A, Structure Of The Clostridium Botulinum C3 Exoen
(Wild-Type) In Complex With Nad
gi|12084428|pdb|1G24|D **S** Chain D, The Crystal Structure Of Exoenzyme C3 From Clos
Botulinum
gi|12084427|pdb|1G24|C **S** Chain C, The Crystal Structure Of Exoenzyme C3 From Clos
Botulinum
gi|12084426|pdb|1G24|B **S** Chain B, The Crystal Structure Of Exoenzyme C3 From Clos
Botulinum
gi|12084425|pdb|1G24|A **S** Chain A, The Crystal Structure Of Exoenzyme C3 From Clos
Botulinum
Length = 211

Score = 609 bits (1429), Expect = e-173

Identities = 201/213 (94%), Positives = 202/213 (94%), Gaps = 7/213 (3%)

Query: 19 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 78
AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF

Sbjct: 1 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 60

Query: 79 PSNLIKQ--WLLDKSFNKMKTPENIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 136
PSNLIKQ LLDKSFNKMKTPENIMLF GDDPAYLGTEFQNTLLNSNGTINKTAFEKAK

Sbjct: 61 PSNLIKQVE-LLDKSFNKMKTPENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 119

Query: 137 AIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGOLEG-LP 195
A +FLN DRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAF GQLE LP

Sbjct: 120 A-KFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLP 178

Query: 196 RHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
RHSTYHIDDMRLSSDGKQIIITAT GTAINPK

Sbjct: 179 RHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 211

☐ >gi|23200102|pdb|1GZE|D **S** Chain D, Structure Of The Clostridium Botulinum C3 Exo
Mutant)
gi|23200101|pdb|1GZE|C **S** Chain C, Structure Of The Clostridium Botulinum C3 Exoen
Mutant)
gi|23200100|pdb|1GZE|B **S** Chain B, Structure Of The Clostridium Botulinum C3 Exoen
Mutant)
gi|23200099|pdb|1GZE|A **S** Chain A, Structure Of The Clostridium Botulinum C3 Exoen
Mutant)
Length = 211

Score = 599 bits (1407), Expect = e-170

Identities = 200/213 (93%), Positives = 201/213 (94%), Gaps = 7/213 (3%)

Query: 19 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 78
 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF
 Sbjct: 1 AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGF 60

Query: 79 PSNLIQ--WLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 136
 PSNLIQ LLDKSFNKMKTPEINIMLF GDDPAYLGTEFQNTLLNSNGTINKTAFEKAK
 Sbjct: 61 PSNLIQVE--LLDKSFNKMKTPEINIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAK 119

Query: 137 AIQFLNXDRLEYGYISTSMLNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG-LP 195
 A +FLN DRLEYGYISTS MNVSQFAGRPIITKFKVAKGSKAGYIDPISAF GQLE LP
 Sbjct: 120 A-KFLNKDRLEYGYISTSMLNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLP 178

Query: 196 RHSTYHIDDMRLSSDGKQIIITAT--GTAINPK 226
 RHSTYHIDDMRLSSDGKQIIITAT GTAINPK
 Sbjct: 179 RHSTYHIDDMRLSSDGKQIIITATMMGTAINPK 211

☐ >gi|399048|sp|Q00901|ARC3_CBCP Mono-ADP-ribosyltransferase C3 precursor (Exoenzy
 gi|80492|pir||A41021 NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3 precu
 Clostridium botulinum phage (strain C003-9)
 gi|144737|gb|AAA23212.1| C3 ADP-ribosyltransferase
 Length = 244

Score = 338 bits (791), Expect = 2e-91
 Identities = 129/205 (62%), Positives = 163/205 (79%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
 Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG P
 Sbjct: 42 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIFKFTDASKINGPLRANQGNENGLP 101

Query: 80 SNL---IKQWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
 +++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTINKT FE K
 Sbjct: 102 ADILQKVK--LIDQSFSKMKMPQNIILFRGDDPAYLGPEFQDKILNKDGTINKTVFEQVK 159

Query: 135 AKAIQFLNXDRLEYGYISTSMLNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
 AK FL DR EYGYISTSML+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
 Sbjct: 160 AK---FLKKDRTEYGYISTSMLS-AQFGGRPIVTKFKVTNGSKGGYIDPISYFPGQLEVL 215

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
 LPR+++Y+I DM++S + +QI+ITA
 Sbjct: 216 LPRNNSYYISDMQISPNNRQIMITA 240

☐ >gi|56965901|pdb|1R4B|B **S** Chain B, Adp-Ribosyltransferase C3bot2 From Clostridiu
 Monoclinic Form

gi|56965900|pdb|1R4B|A **S** Chain A, Adp-Ribosyltransferase C3bot2 From Clostridium
 Monoclinic Form

gi|56965899|pdb|1R45|D **S** Chain D, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form

gi|56965898|pdb|1R45|C **S** Chain C, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form

gi|56965897|pdb|1R45|B **S** Chain B, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form

gi|56965896|pdb|1R45|A **S** Chain A, Adp-Ribosyltransferase C3bot2 From Clostridium
 Triclinic Form
 Length = 204

Score = 338 bits (791), Expect = 2e-91
Identities = 129/205 (62%), Positives = 163/205 (79%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG P
Sbjct: 2 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLP 61

Query: 80 SNL---IKQWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
+++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTINKT FE K
Sbjct: 62 ADILQKVK--LIDQSFSKMKMPQNIILFRGDDPAYLGPEFQDKILNKDGTINKTVFEQVK 119

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
AK FL DR EYGYISTSLM+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
Sbjct: 120 AK---FLKKDRTEYGYISTSLMS-AQFGGRPIVTKFKVTNGSKGGYIDPISYFPQGQLEVL 175

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
LPR+++Y+I DM++S + +QI+ITA
Sbjct: 176 LPRNNSYYISDMQISPNNRQIMITA 200

☐ >gi|404821|dbj|BAA04492.1| ADP-ribosyltransferase C3 [Clostridium botulinum D]
Length = 244

Score = 328 bits (768), Expect = 1e-88
Identities = 127/205 (61%), Positives = 161/205 (78%), Gaps = 12/205 (5%)

Query: 20 YSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFP 79
Y++T+ EFTN+++AK WGNAQYKKYGLSK E+EAI YT+ AS+ING LR N+G NG
Sbjct: 42 YADTFTEFTNVEEAKKWGNAQYKKYGLSKPEQEAIKFYTRDASKINGPLRANQGNENGLS 101

Query: 80 SNL---IKQWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFE--K 134
S++ +K L+D+SF+KMK P+NI+LF GDDPAYLG EFQ+ +LN +GTIN+ FE K
Sbjct: 102 SDILQKVK--LIDQSFSKMKMPQNIILFRGDDPAYLGPEFQDKILNKDGTINRDVFEQVK 159

Query: 135 AKAIQFLNXDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFQGQLEG- 193
AK FL DR EYGYISTSLM+ +QF GRPI+TKFKV GSK GYIDPIS F GQLE
Sbjct: 160 AK---FLKKDRTEYGYISTSLMS-AQFGGRPIVTKFKVTNGSKGGYIDPISYFPQGQLEVL 215

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
LPR+++Y+I DM++S + +QI+ITA
Sbjct: 216 LPRNNSYYISDMQISPNNRQIMITA 240

☐ >gi|1212875|emb|CAA60674.1| exoenzyme C3 [Clostridium limosum]
gi|2498151|sp|Q46134|ARC3 CLOLM Mono-ADP-ribosyltransferase C3 precursor (Exoenzy
gi|11282305|pir||A46957 NAD+-asparagine ADP-ribosyltransferase (EC 2.4.2.-) C3-li
precursor [validated] - Clostridium limosum phage
Length = 250

Score = 316 bits (739), Expect = 7e-85
Identities = 126/205 (61%), Positives = 160/205 (78%), Gaps = 7/205 (3%)

Query: 18 KAYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVING 77
K Y++++EFTNID+A+AWG+ Q+ KY LS SEK A+ YT++A+ ING LR N+G NG
Sbjct: 45 KPYADSFKEFTNIDEARAWGDKQFAKYKLSSEKNALTIYTRNAARINGPLRANQGNTNG 104

Query: 78 FPSNLIK---QWLLDKSFNKMKTPEINIMLFXGDDPAYLGTEFQNTLLNSNGTINKTAFEK 134
 P+++ K Q +DKSF KM+TPENI+LF GDDP YLG +F+NT+LN +GTINK FE+
 Sbjct: 105 LPADIRKEVEQ--IDKSFTKMQTPEINILFRGDDPGYLGPDFENTILNRDGTINKAVFEQ 162

Query: 135 AKAIQFLNXDRLEYGYISTSIMNVSQFAGRPITKFKVAKGSKAGYIDPISAFQGGLEG- 193
 K ++F DR EYGYISTS+L N S FAGRPITKFKV GSKAGYI+PIS F+GQLE
 Sbjct: 163 VK-LRFKKGDRKEYGYISTSILVNGSAFAGRPITKFKVLDGSKAGYIEPISTFKGQLEVL 221

Query: 194 LPRHSTYHIDDMRLSSDGKQIIITA 218
 LPR STY I DM+++ + KQIIITA
 Sbjct: 222 LPRSSTYTISDMQIAPNNKQIIITA 246

☐ >[gi|22795813|emb|CAD22164.1|](#) ADP-ribosyltransferase [Bacillus cereus]
 Length = 219

Score = 76.6 bits (173), Expect = 1e-12
 Identities = 74/209 (35%), Positives = 108/209 (51%), Gaps = 64/209 (30%)

Query: 28 TNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEIN-----GKL-----RQNKGVI 75
 TN ++A AWG Q+ K+ SK EK AI YTK+A N GKL + K I
 Sbjct: 20 TNKEEADAWGKKQFNKW--SKEEKSAIRDYTKNARPYNEFLRMHAGKLDSDPTMKKK--I 75

Query: 76 NGFPSNLIKQWLLDKSFNKM--KTPENIMLFXGDDPAYL-GTEFQNTLLNSNGTINKTAF 132
 LDK+ N+ K +NI ++ GDD A++ G E+ N+++ NG +++
 Sbjct: 76 ES-----LDKALNRKEAKVNDNIKVYRGDD-AWIFGKEYDNSIIK-NGKVDR--- 120

Query: 133 EKAKAIQ--FLNXDRL-----EYGYISTS-IMNVSQFAG----RPIITKFKVAKGSKAG 179
 EK K IQ F E+GYISTS L++ AG RP++T+FKV G+
 Sbjct: 121 EKFKIEIQKKF-----QGKTTTEFGYISTSILID----AGYAKTRPVMTEFKVGSGTHGA 170

Query: 180 YI--DPISAFQGG---LEGLPRHSTYHID 203
 Y+ D ++A+ GQ L LPR++ Y I+
 Sbjct: 171 YMNSDDLTAYPGQYELL--LPRNTVYKIE 197

☐ >[gi|236587|gb|AAB19984.1|](#) ADP-ribosyltransferase exoenzyme C3 [Clostridium botul
 C strain Stockholm, CST, Peptide Partial, 20 aa]
 Length = 20

Score = 69.8 bits (157), Expect = 1e-10
 Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 19 AYSNTYQEFTNIDQAKAWGN 38
 AYSNTYQEFTNIDQAKAWGN
 Sbjct: 1 AYSNTYQEFTNIDQAKAWGN 20

☐ >[gi|13186140|emb|CAC33493.1|](#) ADP-ribosyltransferase [Staphylococcus aureus]
[gi|34810145|pdb|1OJZ|A](#) ☒ Chain A, The Crystal Structure Of C3stau2 From S. Aureus
 Nad
[gi|34810144|pdb|1OJQ|A](#) ☒ Chain A, The Crystal Structure Of C3stau2 From S. Aureus
 Length = 212

Score = 66.8 bits (150), Expect = 1e-09

Identities = 78/232 (33%), Positives = 113/232 (48%), Gaps = 70/232 (30%)

Query: 27 FTNIDQAKAWGNAQYK--KYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNL-- 82
 FT++ +A WGN+ K KY SK +K AI +YTK++S IN LR G +N N+
 Sbjct: 6 FTDLVEATKWGNSLIKSAKYS-SK-DKMAIYNYTKNSSPINTPLRSANGDVNKLSENIQE 63

Query: 83 -IKQWLLDKSFNKMKTPENI----MLFXGDDPAYLG--TEF-----Q----- 117
 ++Q LD + +K TP+++ +L + YL T F Q
 Sbjct: 64 QVRQ--LDSTISKSVTPDSVYVYRLL----NLDYLSSITGFTREDLHMLQQTNNNGQYNEA 117

Query: 118 -----NTLLNSNGTINKTAFEKAKAIQFLNXDRL--EYGYISTSLMNVSQFAGRPIITKF 170
 N L+NS R+ E GY ST L++ + AGRPI K
 Sbjct: 118 LVSKLNNLMNS-----RIYRENGYSSTQLVSGAALAGRPIELKL 156

Query: 171 KVAKGSKAGYIDP--ISAFQGQLEG-LPRHSTYHIDDMRLSSDGKQ-IIITA 218
 ++ KG+KA YID ++A+ GQ E LPR + Y + ++L SD K+ IIITA
 Sbjct: 157 ELPKGTAKAAYIDSKELTAYPGQQEVLLPRGTEYAVGSVKL-SDNKRKIIITA 207

☐ >gi|24636605|dbj|BAC22946.1| epidermal cell differentiation inhibitor B [Staphyl
 Length = 247

Score = 66.8 bits (150), Expect = 1e-09

Identities = 78/232 (33%), Positives = 113/232 (48%), Gaps = 70/232 (30%)

Query: 27 FTNIDQAKAWGNAQYK--KYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNL-- 82
 FT++ +A WGN+ K KY SK +K AI +YTK++S IN LR G +N N+
 Sbjct: 41 FTDLVEATKWGNSLIKSAKYS-SK-DKMAIYNYTKNSSPINTPLRSANGDVNKLSENIQE 98

Query: 83 -IKQWLLDKSFNKMKTPENI----MLFXGDDPAYLG--TEF-----Q----- 117
 ++Q LD + +K TP+++ +L + YL T F Q
 Sbjct: 99 QVRQ--LDSTISKSVTPDSVYVYRLL----NLDYLSSITGFTREDLHMLQQTNNNGQYDEA 152

Query: 118 -----NTLLNSNGTINKTAFEKAKAIQFLNXDRL--EYGYISTSLMNVSQFAGRPIITKF 170
 N L+NS R+ E GY ST L++ + AGRPI K
 Sbjct: 153 LVSKLNNLMNS-----RIYRENGYSSTQLVSGAALAGRPIELKL 191

Query: 171 KVAKGSKAGYIDP--ISAFQGQLEG-LPRHSTYHIDDMRLSSDGKQ-IIITA 218
 ++ KG+KA YID ++A+ GQ E LPR + Y + ++L SD K+ IIITA
 Sbjct: 192 ELPKGTAKAAYIDSKELTAYPGQQEVLLPRGTEYAVGSVKL-SDNKRKIIITA 242

☐ >gi|80491|pir||S05236 exoenzyme C3 - Clostridium botulinum (fragment)
 Length = 22

Score = 61.7 bits (138), Expect = 4e-08

Identities = 21/23 (91%), Positives = 21/23 (91%), Gaps = 2/23 (8%)

Query: 19 AYSNTYQEF-TNIDQAKAWGNAQ 40
 AYSNTYQEF TNIDQAKA GNAQ
 Sbjct: 1 AYSNTYQEFNTNIDQAKA-GNAQ 22

☐ >gi|236588|gb|AAB19985.1| ADP-ribosyltransferase exoenzyme C3 [Clostridium botul
 D strain D1873, Peptide Partial, 20 aa]
 Length = 20

Score = 59.6 bits (133), Expect = 2e-07
Identities = 19/20 (95%), Positives = 19/20 (95%)

Query: 19 AYSNTYQEFTNIDQAKAWGN 38
AYSNTYQEFTNIDQAKA GN
Sbjct: 1 AYSNTYQEFTNIDQAKAXGN 20

☐ >gi|17227179|ref|NP_478345.1| hypothetical protein [Staphylococcus aureus]
gi|17148579|dbj|BAB78400.1| ORF2~epidermal cell differentiation inhibitor C of St
aureus
Length = 247

Score = 59.2 bits (132), Expect = 2e-07
Identities = 35/75 (46%), Positives = 49/75 (65%), Gaps = 7/75 (9%)

Query: 147 EYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDP--ISAFQGG---LEGLPRHSTYH 201
EYGY ST L+ + AGRPI K ++ KG+KA YID ++A+ GQ L LPR + Y
Sbjct: 168 EYGYSTQLVKGAALAGRPIELKLQLPKGTAAAYIDSKNLTAYPGQQEIL--LPRGTDYT 225

Query: 202 IDDMRLSSDGKQIII 216
I+ ++LS D K+I+I
Sbjct: 226 INTVKLSDDHKRILI 240

Score = 43.9 bits (96), Expect = 0.008
Identities = 26/61 (42%), Positives = 37/61 (60%), Gaps = 10/61 (16%)

Query: 27 FTNIDQAKAWGN-----AQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNGVINGFPSN 81
FT++ +A WGN A Y SK +KEAI +YTK +S IN LR ++G I+ F ++
Sbjct: 41 FTDLTEATNWGNKLIKQANYS----SK-DKEAIYNYTKYSSPINTPLRSSQGDISNFSAD 95

Query: 82 L 82
L
Sbjct: 96 L 96

☐ >gi|79857|pir||JG0016 epidermal cell differentiation inhibitor precursor - Staph
aureus
gi|119131|sp|P24121|EDIN STAAU Epidermal cell differentiation inhibitor precursor
gi|152998|gb|AAA26616.1| epidermal cell differentiation inhibitor
Length = 247

Score = 53.2 bits (118), Expect = 1e-05
Identities = 89/261 (34%), Positives = 119/261 (45%), Gaps = 93/261 (35%)

Query: 13 YSFNQK--AYSNTY-----QEFTNIDQAKAWGNAQYK-----KYGLSKSEKEAIVSYTKS 60
YS N K SNT + FT++D+A WGN K KY S +K A+ YTK
Sbjct: 20 YSINDKIIIEVSNTSLAADVKNFDTLDEATKWGN---KLIKQAKY--SSDDKIALYEYTKD 74

Query: 61 ASEINGKLRQNGVINGFPSNLIKQWL-----LDKSFNKMKTPENI----ML--- 103
+S+ING LR G IN K L LD S +K TPE++ +L
Sbjct: 75 SSKINGPLRLAGGDIN-----K--LDSTTQDKVRRLDSSISKSTTPESVYVYRLLNLD 125

Query: 104 -----FXGDDPAY-LGTEFQNTLLNSNGTINKTAFEKAKAIQF-----LN---XDR 145